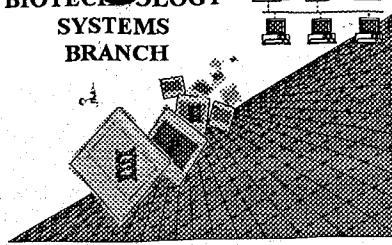


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/807,248
Source: OIPE
Date Processed by STIC: 7/19/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/807248

ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPHA" IIHEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic Acid
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped.
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/807,248

DATE: 07/19/2001
TIME: 12:23:45

Input Set : A:\BB1208pct seq 1st.txt
Output Set: N:\CRF3\07192001\I807248.raw

3 <110> APPLICANT: E. I. du Pont de Nemours and Company
5 <120> TITLE OF INVENTION: SCORPION TOXINS
7 <130> FILE REFERENCE: BB1208
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/807,248
C--> 10 <141> CURRENT FILING DATE: 2001-06-27
12 <150> PRIOR APPLICATION NUMBER: 60/105,404
13 <151> PRIOR FILING DATE: 1998-10-23
15 <160> NUMBER OF SEQ ID NOS: 17
17 <170> SOFTWARE: Microsoft Office 97

Does Not Comply
Corrected Diskette Needed

pp 1-2

ERRORED SEQUENCES

55 <210> SEQ ID NO: 3
56 <211> LENGTH: 238
57 <212> TYPE: DNA
58 <213> ORGANISM: Leiurus quinquestriatus
60 <400> SEQUENCE: 3 see item 9 on Error Summary Sheet
E--> 61 tagtttggca cttcttca tgacaggggt ggagagtgtc cgtgacgggtt atattgc当地 60
62 gcccggaaac tttgcacacc attgtttcc agggccttcc gtttgc当地 cattatgtaa 120
63 gggaaaacgggt ggtacgggtg gccattgc当地 atttaaagggt ggacatggaa ctgc当地ctgctg 180
64 gtgcaatgcc ttgccc当地ata aagttagggat tatagtagat ggagtaaaat gccatcg 238
155 <210> SEQ ID NO: 8
156 <211> LENGTH: 252
157 <212> TYPE: DNA
158 <213> ORGANISM: Leiurus quinquestriatus
160 <400> SEQUENCE: 8 see item 9
E--> 161 atgaattattt tggtaggtat tagtttggca cttcttca tgacaggggt ggagagtgg 60
162 cgtgatgctt atattgc当地 gaactataac tttgttatatc attgtgtttt aaatccat 120
163 tgcaacgatt tatgtaccaa gaacgggtct aagagtggct attgccaatg gttc当地gttca 180
164 agtggaaacg cctgtgggtg catagatttgc cccgataacg taccgattaa agtaccagg 240
165 aaatgc当地tc gc

see next page

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<210> 9
<211> 84
<212> PRT
<213> Leiurus quinquestriatus

<220>
<221> SIGNAL
<222> (1)..(19)

<400> 9

Met Asn Tyr Leu Val Xaa Ile Ser Leu Ala Leu Leu Leu Met Thr Gly
1 5 10 15

Val Glu Ser Gly Arg Asp Ala Tyr Ile Ala Gln Asn Tyr Asn Cys Val
20 25 30

Tyr His Cys Ala Leu Asn Pro Tyr Cys Asn Asp Leu Cys Thr Lys Asn
35 40 45

Gly Ala Lys Ser Gly Tyr Cys Gln Trp Phe Gly Ser Ser Gly Asn Ala
50 55 60

Cys Trp Cys Ile Asp Leu Pro Asp Asn Val Pro Ile Lys Val Pro Gly
65 70 75 80

Lys Cys His Arg

item 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/807,248

DATE: 07/19/2001

TIME: 12:23:46

Input Set : A:\BB1208pct seq 1st.txt
Output Set: N:\CRF3\07192001\I807248.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:61 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:161 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:177 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9